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RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

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#25

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/446,089C

Source: 1638 RUST

Date Processed by STIC: 6/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/446,089C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
 Sequence(s) 10 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/446,089C

DATE: 06/20/2001

TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\06202001\I446089C.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: SAKAKIBARA, Keiko
4 FUKUI, Yuko
5 TANAKA, Yoshikazu
6 KUSUMI, Takaaki
7 MIZUTANI, Masako
8 NAKAYAMA, Toru
10 <120> TITLE OF INVENTION: GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY
12 <130> FILE REFERENCE: 001560-377
14 <140> CURRENT APPLICATION NUMBER: US 09/446,089C
15 <141> CURRENT FILING DATE: 1999-12-17
17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02045
18 <151> PRIOR FILING DATE: 1999-04-16
20 <150> PRIOR APPLICATION NUMBER: JP 10/107296
21 <151> PRIOR FILING DATE: 1998-04-17
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1951
29 <212> TYPE: DNA
30 <213> ORGANISM: Antirrhinum majus
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (96)..(1781)
36 <400> SEQUENCE: 1
37 aaattacatt gcttccttg tccccaccc caccaccaat atatacaact tcctcagcta 60
39 gttgtttatt atcaaatcaaa taaaattatt tccca atg ttc aaa aat cct aat 113
40 Met Phe Lys Asn Pro Asn
41 1 5
43 atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161
44 Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
45 10 15 20
47 tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209
48 Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
49 25 30 35
51 cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257
52 Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
53 40 45 50
55 ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305
56 Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
57 55 60 65 70
59 tgt ggt cag cca gac ttg cca cct ggc aca gca cca ata aac tgt tgt 353
60 Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
61 75 80 85
63 ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc 401
64 Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser
65 90 95 100
67 act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac 449

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,089C

DATE: 06/20/2001
TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\06202001\I446089C.raw

68	Thr	Thr	Met	Arg	Val	Arg	Ala	Ala	His	Leu	Val	Asp	Asp	Ala	Tyr		
69			105				110				115						
71	att	gcc	aaa	ttc	aag	aaa	gcc	gtt	gag	ctt	atg	cga	gct	cta	cct	gag	497
72	Ile	Ala	Lys	Phe	Lys	Lys	Ala	Val	Glu	Leu	Met	Arg	Ala	Leu	Pro	Glu	
73			120				125			130							
75	gat	gac	cct	cgt	agc	ttc	aag	caa	caa	gct	aac	gtc	cat	tgc	gct	tac	545
76	Asp	Asp	Pro	Arg	Ser	Phe	Lys	Gln	Gln	Ala	Asn	Val	His	Cys	Ala	Tyr	
77	135					140				145			150				
79	tgc	gct	ggg	gct	tat	aat	caa	gcc	ggt	ttc	aca	aac	cta	aag	ctc	caa	593
80	Cys	Ala	Gly	Ala	Tyr	Asn	Gln	Ala	Gly	Phe	Thr	Asn	Leu	Lys	Leu	Gln	
81			155				160			165							
83	atc	cac	cga	tct	tgg	ctt	ttt	ttc	ccg	ttc	cat	aga	tat	tat	atc	tac	641
84	Ile	His	Arg	Ser	Trp	Leu	Phe	Phe	Pro	Phe	His	Arg	Tyr	Tyr	Ile	Tyr	
85			170				175			180							
87	ttt	ttt	gaa	aga	ata	ttg	gga	aaa	cta	atc	aat	gat	aca	act	ttt	gct	689
88	Phe	Phe	Glu	Arg	Ile	Leu	Gly	Lys	Leu	Ile	Asn	Asp	Thr	Thr	Phe	Ala	
89			185				190			195							
91	ctc	caa	ttt	tgg	aac	tat	gat	tca	cct	ggt	gga	atg	aca	atc	cca	tca	737
92	Leu	Gln	Phe	Trp	Asn	Tyr	Asp	Ser	Pro	Gly	Gly	Met	Thr	Ile	Pro	Ser	
93			200				205			210							
95	atg	ttt	att	gat	act	aat	tct	tgc	ctg	tac	gat	agt	tta	cggt	gac	agt	785
96	Met	Phe	Ile	Asp	Thr	Asn	Ser	Ser	Leu	Tyr	Asp	Ser	Leu	Arg	Asp	Ser	
97	215					220			225			230					
99	aat	cat	cag	cca	cca	acc	atc	gta	gac	ttg	aac	tac	gcc	ttt	tct	gat	833
100	Asn	His	Gln	Pro	Pro	Thr	Ile	Val	Asp	Leu	Asn	Tyr	Ala	Phe	Ser	Asp	
101						235			240			245					
103	tcc	gac	aat	acc	act	act	cct	gaa	gag	caa	atg	att	ata	aac	ctt	aaa	881
104	Ser	Asp	Asn	Thr	Thr	Pro	Glu	Glu	Gln	Met	Ile	Ile	Asn	Leu	Lys		
105						250			255			260					
107	att	gtg	tac	aga	caa	atg	gtg	tgc	agc	gct	aag	act	cca	cag	ctt	ttc	929
108	Ile	Val	Tyr	Arg	Gln	Met	Val	Ser	Ser	Ala	Lys	Thr	Pro	Gln	Leu	Phe	
109						265			270			275					
111	tcc	ggc	cgc	cca	tac	cga	cgt	ggg	gac	caa	gag	ttt	ccc	ggg	gtg	ggg	977
112	Phe	Gly	Arg	Pro	Tyr	Arg	Arg	Gly	Asp	Gln	Glu	Phe	Pro	Gly	Val	Gly	
113						280			285			290					
115	tcg	att	gag	tta	gtc	cct	cat	ggc	atg	ata	cat	tta	tgg	acc	ggt	tct	1025
116	Ser	Ile	Glu	Leu	Val	Pro	His	Gly	Met	Ile	His	Leu	Trp	Thr	Gly	Ser	
117						295			300			305			310		
119	gag	aac	acg	ccc	tat	ggc	gag	aac	atg	ggg	gct	ttc	tac	tca	acg	gct	1073
120	Glu	Asn	Thr	Pro	Tyr	Gly	Glu	Asn	Met	Gly	Ala	Phe	Tyr	Ser	Thr	Ala	
121						315			320			325					
123	aga	gac	ccg	ata	ttt	ttt	gct	cat	cat	tcg	aac	gtc	gat	aga	atg	tgg	1121
124	Arg	Asp	Pro	Ile	Phe	Phe	Ala	His	His	Ser	Asn	Val	Asp	Arg	Met	Trp	
125						330			335			340					
127	tcc	ata	tgg	aag	acc	cta	gga	ggg	ccg	ccg	agg	acg	gac	tta	aca	gat	1169
128	Ser	Ile	Trp	Lys	Thr	Leu	Gly	Gly	Pro	Arg	Arg	Thr	Asp	Leu	Thr	Asp	
129						345			350			355					
131	cca	gat	ttt	ctt	gat	gct	tct	ttc	gtt	ttt	tat	gac	gaa	aac	gca	gag	1217
132	Pro	Asp	Phe	Leu	Asp	Ala	Ser	Phe	Val	Phe	Tyr	Asp	Glu	Asn	Ala	Glu	

RAW SEQUENCE LISTING
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DATE: 06/20/2001
TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\06202001\I446089C.raw

133	360	365	370														
135	atg	gtt	cggttc	aag	gtt	cggttc	gat	tgc	tta	gat	gaa	aag	aaa	ctatgg	1265		
136	Met	Val	Arg	Val	Lys	Val	Arg	Asp	Cys	Leu	Asp	Glu	Lys	Lys	Leu	Gly	
137	375																
139	tac	gtt	tat	caa	gat	gtgt	gag	att	ccgttc	ctc	aac	act	cgt	ccatca	1313		
140	Tyr	Val	Tyr	Gln	Asp	Val	Glu	Ile	Pro	Trp	Leu	Asn	Thr	Arg	Pro	Thr	
141																	
143	cca	aaa	gtt	tct	ccgttc	ctat	ctt	aag	aaa	ttt	cat	aga	aca	aac	act	1361	
144	Pro	Lys	Val	Ser	Pro	Ser	Leu	Leu	Lys	Lys	Phe	His	Arg	Thr	Asn	Thr	
145																	
147	gcc	aat	ccgttc	aga	caa	gtt	ttt	ccgttc	gat	ata	ctt	gac	aga	gtctta	1409		
148	Ala	Asn	Pro	Arg	Gln	Val	Phe	Pro	Ala	Ile	Leu	Asp	Arg	Val	Leu	Lys	
149																	
151	gtt	atc	gtgt	acgttc	agg	ccgttc	aag	aaa	act	aga	agt	agg	aaa	gaa	aag	gac	1457
152	Val	Ile	Val	Thr	Arg	Pro	Lys	Lys	Thr	Arg	Ser	Arg	Lys	Glu	Lys	Asp	
153																	
155	gag	tta	gaa	gag	att	tta	gtgt	att	gaa	ggg	att	gaa	ctgt	gaa	aga	gac	1505
156	Glu	Leu	Glu	Glu	Ile	Leu	Val	Ile	Glu	Gly	Ile	Glu	Leu	Glu	Arg	Asp	
157																	
159	cac	ggg	cac	gtatcc	gac	gtt	tat	att	aat	gct	gac	gaa	gat	gac		1553	
160	His	Gly	His	Val	Lys	Phe	Asp	Val	Tyr	Ile	Asn	Ala	Asp	Glu	Asp	Asp	
161																	
163	ctt	gcc	gtgt	att	tcc	ccgttc	gag	aat	gct	gag	ttc	gcc	ggg	agt	ttcgtgt	1601	
164	Leu	Ala	Val	Ile	Ser	Pro	Glu	Asn	Ala	Glu	Phe	Ala	Gly	Ser	Phe	Val	
165																	
167	agt	ctgt	tgg	cac	aaa	cct	ata	aag	ggg	aag	agg	aca	aag	acgttc	tta	1649	
168	Ser	Leu	Trp	His	Lys	Pro	Ile	Lys	Gly	Lys	Arg	Thr	Lys	Thr	Gln	Leu	
169																	
171	tta	aca	ttgt	tgc	att	tgt	gat	att	ttgt	gag	gat	ttgt	gat	gct	gac	gaa	1697
172	Leu	Thr	Leu	Ser	Ile	Cys	Asp	Ile	Leu	Glu	Asp	Leu	Asp	Ala	Asp	Glu	
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175	gat	gat	tat	gtgt	ttgt	gtc	act	ttgt	ccgttc	gag	aac	gcc	gga	gat	gct	1745	
176	Asp	Asp	Tyr	Val	Leu	Val	Thr	Leu	Val	Pro	Arg	Asn	Ala	Gly	Asp	Ala	
177																	
179	atc	aag	att	cat	aat	gtc	aag	att	gag	ctt	gat	ggc	taataaaattc		1791		
180	Ile	Lys	Ile	His	Asn	Val	Lys	Ile	Glu	Leu	Asp	Gly					
181																	
183	tattgatttc	ttctcaacct	acagttgatc	atttaccgat	tgattattcc	aataaaagta									1851		
185	tctcatgtac	caatatcgat	cgttataatc	gtaataacttt	cagattttta	tttattttaaa									1911		
187	agcagttgta	taaatggta	aataaggatt	actttttgag											1951		
190	<210>	SEQ	ID	NO:	2												
191	<211>	LENGTH:	562														
192	<212>	TYPE:	PRT														
193	<213>	ORGANISM:	Antirrhinum majus														
195	<400>	SEQUENCE:	2														
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198	1						5			10				15			
201	Asn	Asp	Asn	Asp	Gln	Glu	Ser	Ser	His	Arg	Cys	Lys	His	Ile	Leu		
202														30			

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,089C

DATE: 06/20/2001
TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\06202001\I446089C.raw

205 Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
206 35 40 45
209 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
210 50 55 60
213 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
214 65 70 75 80
217 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
218 85 90 95
221 Glu Leu Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
222 100 105 110
225 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
226 115 120 125
229 Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
230 130 135 140
233 Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
234 145 150 155 160
237 Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
238 165 170 175
241 His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
242 180 185 190
245 Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
246 195 200 205
249 Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
250 210 215 220
253 Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
254 225 230 235 240
257 Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Pro Glu Glu Gln
258 245 250 255
261 Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
262 260 265 270
265 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
266 275 280 285
269 Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
270 290 295 300
273 His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
274 305 310 315 320
277 Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
278 325 330 335
281 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
282 340 345 350
285 Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
286 355 360 365
289 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
290 370 375 380
293 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
294 385 390 395 400
297 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
298 405 410 415
301 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,089C

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TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\06202001\I446089C.raw

302	420	425	430
305	Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg		
306	435	440	445
309	Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly		
310	450	455	460
313	Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile		
314	465	470	475
317	Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu		
318	485	490	495
321	Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys		
322	500	505	510
325	Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu		
326	515	520	525
329	Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro		
330	530	535	540
333	Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu		
334	545	550	555
337	Asp Gly		560
341	<210> SEQ ID NO: 3		
342	<211> LENGTH: 13		
343	<212> TYPE: PRT		
344	<213> ORGANISM: Antirrhinum majus		
346	<400> SEQUENCE: 3		
348	Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro		
349	1	5	10
352	<210> SEQ ID NO: 4		
353	<211> LENGTH: 12		
354	<212> TYPE: PRT		
355	<213> ORGANISM: Antirrhinum majus		
357	<400> SEQUENCE: 4		
359	Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys		
360	1	5	10
362	<210> SEQ ID NO: 5		
363	<211> LENGTH: 18		
364	<212> TYPE: PRT		
365	<213> ORGANISM: Antirrhinum majus		
367	<400> SEQUENCE: 5		
369	Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln		
370	1	5	10
372	Glu Phe		15
375	<210> SEQ ID NO: 6		
376	<211> LENGTH: 29		
377	<212> TYPE: PRT		
378	<213> ORGANISM: Antirrhinum majus		
380	<220> FEATURE:		
381	<221> NAME/KEY: UNSURE		
382	<222> LOCATION: (8)...(8)		
383	<223> OTHER INFORMATION: Amino acid 8 is Xaa wherein Xaa = unknown or other.		
385	<220> FEATURE:		

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

09/446,089C 6

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<400> 10

His Ala Val Cys Asn Glu
1 5

see item 11 on Enr Summary Sheet

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/446,089C

DATE: 06/20/2001
TIME: 11:02:48

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\06202001\I446089C.raw

L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:466 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:466 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13